OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.4_p5_4578
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Run on: March 15, 2003, 23:25:27 ; Search time 103.105 Seconds
(without alignments)
2525.515 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5
Fgapop  6.0 , Fgapext  7.0
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Searched: 501302 seqs, 350932545 residues

Total number of hits satisfying chosen parameters: 1002604

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Minimum DB seq length: 0
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6	1712	86.2	10	US-09-922-217-1105	Sequence 1105, Ap
7	1712	86.2	10	US-09-925-301-207	Sequence 207, App
8	928.5	46.8	10	US-10-025-380-853	Sequence 853, App
9	928.5	46.8	10	US-09-922-217-853	Sequence 853, App
10	928.5	46.8	10	US-10-025-380-944	Sequence 944, App
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13	833.5	42.0	10	US-09-833-263-853	Sequence 853, App
14	833.5	42.0	10	US-10-076-287A-282	Sequence 282, App
15	803	40.5	10	US-10-007-805-282	Sequence 282, App
16	803	40.5	10	US-09-998-998-2290	Sequence 2290, Ap
17	803	40.5	10	US-09-998-598-2290	Sequence 2290, Ap
18	803	40.5	10	US-09-764-864-320	Sequence 320, App
19	803	40.5	10	US-09-925-297-309	Sequence 309, App
20	803	40.5	10	US-09-998-814-44	Sequence 44, Appl
21	803	40.5	10	US-09-759-143-44	Sequence 44, Appl
22	803	40.5	10	US-09-780-669-44	Sequence 44, Appl
23	765	38.5	10	US-09-030-606-44	Sequence 44, Appl
24	590.5	29.7	9	US-09-822-827-44	Sequence 44, Appl
25	585	29.5	10	US-09-115-453-44	Sequence 44, Appl
26	555.5	28.0	9	US-09-867-701-4818	Sequence 4818, Ap
27	543	27.4	10	US-09-974-298-12	Sequence 12, A
28	543	27.4	10	US-09-960-352-11873	Sequence 11873, A
29	543	27.4	10	US-09-998-598-32	Sequence 32, Appl
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31	543	27.4	10	US-09-864-761-31274	Sequence 31274, A
32	527.5	26.6	9	US-09-998-598-1740	Sequence 1740, Ap
33	442	22.3	9	US-09-998-841-44	Sequence 44, Appl
34	435	21.9	10	US-09-960-352-11873	Sequence 11873, A
35	363	18.3	10	US-09-998-598-32	Sequence 32, Appl
36	290	14.6	10	US-09-864-761-14745	Sequence 14745, A
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39	235	11.8	9	US-10-098-841-45	Sequence 45, Appl
40	234.5	11.8	9	US-10-098-772-3	Sequence 3, Appli
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42	233.5	11.8	10	US-09-126-945B-1	Sequence 1, Appli
43	228	11.5	10	US-09-866-356-2	Sequence 2, Appli
44	225	11.3	10	US-09-962-832-111	Sequence 111, App
44	225	11.3	10	US-09-902-772-1	Sequence 1, Appli
45	222	11.2	9	US-10-015-219-489	Sequence 489, App

SUMMARIES

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1	1712	86.2	1915	10	US-09-964-8244-101	Sequence 101, App
2	1712	86.2	1915	10	US-09-964-8244-563	Sequence 563, App
3	1712	86.2	1915	10	US-08-880-107-3420	Sequence 3420, Ap
4	1712	86.2	1915	10	US-09-967-768A-192	Sequence 192, App

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

RESULT 1
US-09-964-8244-101
Sequence 101, Application US/09964824A
Patent No. US2002010253141A1
GENERAL INFORMATION:
  APPLICANT: Horrigan, Stephen
  TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu...
  TITLE OF INVENTION: Sets
  FILE REFERENCE: 689290-73
  CURRENT APPLICATION NUMBER: US/09/964,824A
  CURRENT FILING DATE: 2001-09-27
  PRIOR APPLICATION NUMBER: US/60/236,028
  PRIOR FILING DATE: 2000-09-28
  PRIOR APPLICATION NUMBER: US/60/236,033
  PRIOR FILING DATE: 2000-09-28
  PRIOR APPLICATION NUMBER: US/60/236,032
  PRIOR FILING DATE: 2000-09-28
  NUMBER OF SEQ ID NOS: 583
  SOFTWARE: Patentin version 3.0
  SEQ ID NO 101
  LENGTH: 1915
  TYPE: DNA
  ORGANISM: Homo sapiens
US-09-964-8244-101

ALIGNMENTS

Alignment Scores:
Pred. No.: 2.42e-172
Pred.: 1712.00
Length: 1915
Matches: 323

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Percent Similarity:    92.74%              Conservative:    22
Best Local Similarity: 86.83%              Mismatches:      25
Query Match:           86.25%              Indels:          2
DB:                    10                  Gaps:            2

US-08-978-217-16 (1-371) x US-09-964-824A-101 (1-1915)

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Db    120 ATGGCTGCAACCTGTGAGATTAGCAACATTTTTAGCAACTACTTCAGTGCGATGTACAGC  179

Qy     21 SerGluAspProThrLeuAlaProAlaProPro---ThrThrPheGlyThrGluAspLeu   39
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Db    180 TCGGAGGACTCCACCCTCGTTCCCCCTGCCCCA---GACCACTTTTGGGACGGGATGACTTG 239

Qy     40 ValLeuThrLeuAsnAsnGlnGlnMetThrLeuGluGluGlyProGlyLysAlaSerTrpThr 59
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Db    300 GGGGAACAGCCCCAGTTCTGGTCGAAGACCCAGGTTCTGGAGTGGATCAGCTACCAAGTG  359

Qy     80 GluLysAsnLysTyrAspAlaSerSerIleAspPheSerArgCysAsnMetAspGlyAla   99
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Db    420 ACCCTCTGCAATTGTGCCCTTGAGGAGCTCGGTCTCGTTTTTGGGCCTCTCGGGGACCAA   479

Qy    120 LeuHisAlaGlnLeuArgAspLeuThrSerAsnSerSerAspGluLeuSerTrpIleIle   139
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Qy    140 GluLeuLeuGluLysAspGlyMetSerProPheGlnLeuSerLeuGlyAspLeuProPhe   159
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Qy    160 AspGlnGlySerProPheAlaGlnGluLeuLeuAspAspGlyArgGlnAlaSerProTyr   179
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Qy    200 ArgThrAlaThrProGlnSerSerHisSerAlaSerGluSerGlyGlySerAspValAspLeu 219
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Db    717 GGGACTGCGGTCACCTCCCACTCCTTCAGACTCCGGTGAGAGTGGAGGTTCAGATGTGGACCTG 776

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Qy    300 GluGlyValPheLeuArgSerGluGluAlaValAlaGlnLeuLeuTrpGlyGlyLysLys   319
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Db   1077 AAGAACAGCAACATGACCTACGAGAAGAAGAGCCGGGGCCCATGAGGTACTACTACAAACGG 1136

Qy    340 GluIleLeuGluArgValAspGlyArgArgLeuValThrTyrLysPheGlyLysAsnSerSer 359
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US-09-964-824A-563
; Sequence 563, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
;  APPLICANT: Horrigan, Stephen
;  TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu...
;  TITLE OF INVENTION: Sets
;  FILE REFERENCE: 689290-73
;  CURRENT APPLICATION NUMBER:
;  CURRENT FILING DATE: 2001-09-27
;  PRIOR APPLICATION NUMBER: US/09/964,824A
;  PRIOR FILING DATE: 2000-09-28
;  PRIOR APPLICATION NUMBER: US/60/236,032
;  PRIOR FILING DATE: 2000-09-28
;  PRIOR APPLICATION NUMBER: US/60/236,033
;  PRIOR FILING DATE: 2000-09-28
;  PRIOR APPLICATION NUMBER: US/60/236,028
;  PRIOR FILING DATE: 2000-09-28
;  NUMBER OF SEQ ID NOS: 583
;  SOFTWARE: Patentin version 3.0
;  SEQ ID NO 563
;  LENGTH: 1915
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-09-964-824A-563

Alignment Scores:
Pred. No.:
Score:                 2.42e-172
Percent Similarity:    1712.00           Length:          1915
Best Local Similarity: 92.74%            Matches:         323
Query Match:           86.83%            Conservative:    22
DB:                    86.25%            Mismatches:      25
                       10                Indels:          2
                                         Gaps:            2

US-08-978-217-16 (1-371) x US-09-964-824A-563 (1-1915)

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Db    120 ATGGCTGCAACCTGTGAGATTAGCAACATTTTTAGCAACTACTTCAGTGCGATGTACAGC  179

Qy     21 SerGluAspProThrLeuAlaProAlaProPro---ThrThrPheGlyThrGluAspLeu   39
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Db    180 TCGGAGGACTCCACCCTCGTTCCCCCTGCCCCA---GACCACTTTTGGGACGGGATGACTTG 239

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Db    240 GTACTGACCCTGAGCAACCCCCAGATGTCATTGGAGGGTACAGAGAGGCCAGCTGGTTG   299

Qy     60 SerGluArgProGlnPheTrpSerLysThrGlnValLeuGluTrpIleSerTyrGlnVal   79
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Db    300 GGGGAACAGCCCCAGTTCTGGTCGAAGACCCAGGTTCTGGAGTGGATCAGCTACCAAGTG  359

Qy     80 GluLysAsnLysTyrAspAlaSerSerIleAspPheSerArgCysAsnMetAspGlyAla   99
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Db    360 GAGAAGAACAAGTACGACGCAAGCAGCCCATTGACTTCTCACGATGTGACATGGATGGCGCC 419

Qy    100 ThrLeuCysSerCysAlaLeuGluLeuGlyLeuValPheGlyProLeuGlyAspGln     119
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Db    420 ACCCTCTGCAATTGTGCCCTTGAGGAGCTCGGTCTCGTTTTTGGGCCTCTCGGGGACCAA   479

Qy    120 LeuHisAlaGlnLeuArgAspLeuThrSerAsnSerSerAspGluLeuSerTrpIleIle   139
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Sequence 3420, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
   APPLICANT: Horne, Darci T.
   APPLICANT: Vockley, Joseph G.
   APPLICANT: Scherf, Uwe
   APPLICANT: Gene Logic, Inc.
   TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
   FILE REFERENCE: 44921-5028-WO
   CURRENT APPLICATION NUMBER: US/09/880,107
   CURRENT FILING DATE: 2001-06-14
   PRIOR APPLICATION NUMBER: US 60/211,379
   PRIOR FILING DATE: 2000-06-14
   PRIOR APPLICATION NUMBER: US 60/237,054
   PRIOR FILING DATE: 2000-10-02
   NUMBER OF SEQ ID NOS: 3950
   SOFTWARE: Patentin Ver. 2.1
   SEQ ID NO 3420
   LENGTH: 1915
   TYPE: DNA
   ORGANISM: Homo sapiens
   FEATURE:
   OTHER INFORMATION: Genbank Accession No. US20020142981A1 U73843
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US-09-880-107-3420

Alignment Scores:
Pred. No.:
Score:                  2.42e-172
                        1712.00                 Length:              1915
Percent Similarity:     92.74%                  Matches:             323
Best Local Similarity:  86.83%                  Conservative:        22
Query Match:            86.25%                  Mismatches:          25
DB:                     10                      Indels:              2
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US-08-978-217-16 (1-371) x US-09-880-107-3420 (1-1915)
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Qy    21  SerGluAspProThrLeuAlaProAlaProPro---ThrThrPheGlyThrGluAspLeu   39
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Db   180  TCGGAGGACCCCACCCTGGCCCCTGCTCCTCCGACCACCTTTGGCCGATGACTTG   239

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Db   240  GTACTGACCCTGAACAACCAGATGACTCTGGAAGGCCCAGGGAAAGCCAGCTGGTTG   299

Qy    60  SerGluArgProGlnPheTrpSerLysTyrAspHisAspGlyAsnGlyAla   79
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Db   300  GAGAGAACAGACCCCCAGTTCTGGTCCAAGTACGACCATGACGGTAACGGAGCC  359

Qy    80  GluLysAsnLysSerTyrAspAlaSerSerIleAspPheSerArgCysAsnMetAspGlyAla   99
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Qy   100  ThrLeuCysSerCysValAlaLeuGluGluLeuArgGluValPheGlyProLeuGlyGln  119
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Db   420  ACCCTCTGCAATTGTGCCCTTGAGGAGCTCCGGGTCTTTGGGCCTCTGGGGCAACCAA   479

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Db   717  GGGACTGGTGCTTCTCCGGAGCTTCCCACTCCTCCGGTGGAAGTGACGTGGACCTG  776

Qy   220  AspLeuThrGluSerLysValPheProArgAspAspPheThrTyrLysLysGlyGlu   239
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Db   777  GATCCCACTGAGTCGCAAGCTCTTCCCCAGCGATGGGTTTCGTGACTGCAAGAAGGGGAT  836

Qy   240  ProLysHisGlyLysArgGlyLysProArgArgLysGluLeuSerLysGluThrTyrTrpAsp  259
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Qy   260  CysLeuGluGlyLysLysSerLysHisAlaProArgGlyThrHisSerLeuTrpGluPhe   279
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Db   897  TGTCTCGAGGGCAAGAAGAGCAAACACGCCCCGCGCGGCACCCACTCGCTGTGGGAGTTCATC  956

Qy   280  ArgAspIleLeuIleHisProGluLeuAsnGluGlyLeuMetLysTrpGluAsnArgHis  299
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Db   957  CGGGACATCCTCATCCACCCGGAGCTCAACGAGGGCCTCATGAAGTGGGAGAATCGGCAT  1016

Qy   300  GluGlyValPheLysPheLeuArgSerGluAlaValAlaGlnLeuLeuTrpGluGlyLysLys  319
          :::
Db  1017  GAAGGGGTCTTCAAGTTCCTGCGCTCCGAGGCTGTGGCCCAACTATGGGAGGGGAA  1076

Qy   320  LysAsnSerAsnMetThrTyrGlyIleLysLysSerArgAlaMetThrArgTyrTyrTyrLysArg  339
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Db  1077  AAGAACAGCAACATGACCTACGGGATCAAGAAGTCTCGGGCCATGACCCGGTACTACTACAAGCGG  1136

Qy   340  GluIleLeuArgValAlaAspGlyArgValTyrLysLysPheGlyLysAsnSerSer   359
          ||||||||||||||||||||||||||||||||||||
Db  1137  GAGATCCTGCGGGTGGCGGACGGCCGGGTGTACAAGTTTGGCAAAAACTCAAGC  1196

Qy   360  GlyTrpProLysGluGluValGlyGluSerArgAsn   371
          |||||||||||||||||||||||:::
Db  1197  GGCTGGCCGAAGGAGGAAGTGGGTGAGAGTCGGAAC  1232
```

RESULT 4
US-09-967-768A-192
; Sequence 192, Application US/09967768A
; Patent No. US20020150877A1
; GENERAL INFORMATION:
; APPLICANT: Augustus, Meena
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-72
; CURRENT APPLICATION NUMBER: US/09/967,768A
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/60/236,109
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,034
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,111
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 192
; LENGTH: 1915
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-967-768A-192

Alignment Scores:
Pred. No.:   2.42e-172   Length: 1915
Score: 1712.00   Matches: 323
Percent Similarity: 92.74%   Conservative: 22
Percent Identity: 86.83%   Mismatches: 25
Best Local Similarity: 86.25%   Indels: 2
Query Match: 10   Gaps: 2
DB:

US-08-978-217-16 (1-371) x US-09-967-768A-192 (1-1915)

| Qy | 1 | MetAlaAlaThrCysGluIleSerAsnValPheSerAsnTyrPheAsnAlaMetTyrSer | 20 |
| Db | 120 | ATGGCTGCAACCTGTGAGATAAGCAACGTATTTTTAGCAAACTACTTCAGTGCCATGTACAGC | 179 |

| Qy | 21 | SerGluAspProThrLeuAlaProLeuAlaProPro--ThrThrPheGlyThrGluAspLeu | 39 |
| Db | 180 | TCGGAGGACTTCCACCCTTGGGCCTTGGGCCGATGGTTG | 239 |

| Qy | 40 | ValLeuThrLeuAsnAsnGlnGlnMetThrLeuGluGlyProGlyLysAlaSerTrpThr | 59 |
| Db | 240 | GTACTGACCCTGAGCAACCCCCAGATGTCATTGGAGGGTACAGAGAAGGCCAGCTGGTTG | 299 |

| Qy | 60 | SerGluArgProGlnProThrProSerLysThrGlnValLeuGlnTrpIleSerTyrGlnVal | 79 |
| Db | 300 | GGGGAACACCCCAGTTCCTGGTCGAAGACCCAGGTTCTGGACTCAGCTACCCAAGTG | 359 |

| Qy | 80 | GluLysAsnLysTyrAspAlaSerIleAspPheSerArgCysAsnMetAspGlyAla | 99 |
| Db | 360 | GAGAAGAACAAGTACCGACACGCAAGCGCCATTGACTTCTCACCGATGGATGGCGCC | 419 |

| Qy | 100 | ThrLeuCysSerCysAlaLeuGluGluLeuValArgLeuValPheGlyProLeuGlyAspGln | 119 |
| Db | 420 | ACCCTCTGCAATTGTGCCCTTGAGGAGCTTCGTCTGGTCTTTGGGCCTCTGGGGGACCAA | 479 |

| Qy | 120 | LeuHisAlaGlnLeuAspLeuThrSerAsnSerSerAspGluLeuSerTrpIleIle | 139 |
| Db | 480 | CTCCATGCCCAGCTGGACCTGAGACCTCACTTCCAGCCTCTTCGATGAGGTCAGTTGGATCATT | 539 |

| Qy | 140 | GluLeuLeuGlyLysAspGlyMetSerPheGlnGluSerLeuGlyProPhe | 159 |
| Db | 540 | GAGCTGCTGGAGAAGGATGGCATGGCCTTCCAGGAGAGCCTA---GACCCAGGGGCCCTT | 596 |

| Qy | 160 | AspGlnGlySerProPheAlaGlnAspLeuLeuAspGlyArgGlnAlaSerProTyr | 179 |
| Db | 597 | GACCAGGGGCAGCCCCTTTGCCCAGGAGCTCTGGACACGACGTCAGCAAGCCAGCCCCTAC | 656 |

| Qy | 180 | TyrCysSerThrThrTyrGlyProGlyAlaProSerProGlySerSerAspValSerThrAla | 199 |
| Db | 657 | CACCCCGGCAGCTGTGGCCGAGGAGCCCCCTCCCCTGGCAGCTCTGACGTTCCACGCA | 716 |

| Qy | 200 | ArgThrAlaThrProGlnSerSerHisAlaSerArgAspSerGlyGlySerAspValAspLeu | 219 |
| Db | 717 | GGGACTGGTGCTTCTGCAGAGGTCCCAACTCCCTCAGACTCCCGTGGAAGTGACGTGGACTTG | 776 |

| Qy | 220 | AspLeuThrGluSerIleValPheProArgAspAspPheThrAspTyrLysLysGlyGlu | 239 |
| Db | 777 | GATCCCACCGACTGAATGGCAAGCTCTTCCCCGGCGATGGTTTTGTGACTCGCAAGAAGGGGAT | 836 |

| Qy | 240 | ProLysHisGlyTyrLysArgArgLysProArgGlyLeuSerGluTyrTyrTyrAsp | 259 |
| Db | 837 | CCCAAACCACGGGATGAGGAGAAGCCCGGGTGTCGAAAAGCCAAGAGAGTACTGGAC | 896 |

| Qy | 260 | CysLeuGluGlyLysLysSerLysHisAlaProArgGlyThrHisLeuPheIle | 279 |
| Db | 897 | TGTCTCGAGGGCAAGAAGAGCAAGCACGCGCCCAGAGGCACCCACCTGTGGGAGTTCATC | 956 |

| Qy | 280 | ArgAspIleLeuIleHisProGluLeuAsnGluGlyLeuMetLysTrpGluAsnArgHis | 299 |
| Db | 957 | CGGGACATCCTCATCCACCCCGAGCTCAACGAGGGCCTCATGAAGTGGGAGAATCGGCAT | 1016 |

| Qy | 300 | GluGlyValPheLysPheLysSerArgGluAlaValAlaGlnLeuLeuTrpGlyGlnLysLys | 319 |
| Db | 1017 | GAAGGGGTCTTCAAGTTCAAGTCCCGCGAGGCTGTGGCCCAACTATGGGGCCAAAAGAAA | 1076 |

| Qy | 320 | LysAsnSerAsnMetThrTyrGlyLeuSerArgAlaMetArgTyrTyrTyrLysLysArg | 339 |
| Db | 1077 | AAGAACAGCAACATGACCTACGGACTAAGCCGGGCCATGAGGTACTACTACAAACGG | 1136 |

| Qy | 340 | GluIleLeuGluArgValAlaAspGlyArgArgLeuValTyrLysPheGlyLysAsnSerSer | 359 |
| Db | 1137 | GAGATCCTGGAACGGGTGGCCGGTGGGGCGGCGACTCGTCTACAAGTTTGGCAAAAACTCAAGC | 1196 |

| Qy | 360 | GlyTrpLysGlyGluGluGluValGlyGluSerArgAsn | 371 |
| Db | 1197 | GGCTGGAAGGGAGGAGAAGAGGTTCTCCAGAGTCGGAAC | 1232 |

RESULT 5
US-10-025-380-1105
; Sequence 1105, Application US/10025380
; Publication No. US20020182191A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.

APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C14
CURRENT APPLICATION NUMBER: US/10/025,380
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 1129
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1105
; LENGTH: 1917
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-025-380-1105

Alignment Scores:
Pred. No.:
Score: 2.42e-172
                                1712.00   Length: 1917
Percent Similarity: 92.74%   Matches: 323
Percent Identity: 86.83%   Conservative: 22
Best Local Similarity: 86.25%   Mismatches: 25
Query Match: 9   Indels: 2
DB: Gaps: 2

US-08-978-217-16 (1-371) x US-10-025-380-1105 (1-1917)

Qy   1   MetAlaAlaThrCysGluIleSerAsnValPheSerAsnTyrPheAsnAlaMetTyrSer   20
           ||||||||||||||||||||||||||| ||:||||||||||||||||||||||||||||
Db   122 ATGGCTGCAACCTGTGAGATTAGCAACAATTTTAGCAACTACTTCAGTCGGATGTACAGC   181

Qy   21   SerGluAspProThrLeuAlaProAlaProPro---ThrThrPheGlyThrGluAspLeu   39
           |||||||||:|||||||||||||||||||| ::|||||||||||||||
Db   182 TCGGAGGACCCAACCCTGGCCCCTGTTCCCCTGCCACCTTTTGGGCGACTTG   241

Qy   40   ValLeuThrLeuAsnAsnGlnIleMetThrLeuGluGlyProGluLysAlaSerTrpThr   59
           ||||||||||||::|||||||||||||||||||||||||||||||||||||||||
Db   242 GTACTGACCCTGAACAACCCCCAGATTGTCATTGGAGGGTACAGAGAAGGCCAGCTGGTTG   301

Qy   60   SerGluArgProGlnPheTrpSerLysThrGlnValLeuGluTrpIleSerTyrGlnVal   79
           |||||||||||||||||||||||||||||||||||::||||||||||||||||||||
Db   302 GGGGAACAGCCCCAGTTCTGGTCGAAGACCCAGGTTCTGGAGTGGATCAGCTACCAAGTG   361

Qy   80   GlyLysAsnLysTyrArgAspAlaSerSerIleAspPheSerSerArgCysAsnMetAspGlyVAla   99
           |||||||||||:::||||||||||:||||||||||||||||||||||||||||||
Db   362 GGAGAGAACAAGTACAGCGACGCCAAGCGCCATTGACTTCTCACGATGTGACATGGATGGGCCC   421

Qy   100 ThrLeuCysSerCysAlaLeuGluGlyLeuLeuArgGlnIleValPheGlyProLeuGlyAspGln   119
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   422 ACCCTCTGCAATTGTGCCCTTGAGGAGCTGCTGCGTCTTTGGGCCCTGGGGACCAA   481

Qy   120 LeuHisAlaGlnLeuArgAspLeuThrSerAsnSerAspGluLeuSerTrpIleIle   139
           |||||||||||||||||||||||||||||||||||||||||||||||
Db   482 CTCCATGCCCAGCTGCGAGACCTCACTTCCAGCTCTCTTGATGAGCTCAGTTGGATCATT   541

Qy   140 GluLeuLeuGluGlyLysAspGlyMetSerPheGlnGluSerLeuGlyIleAspLeuGlyProPhe   159
           |::|||||||||||||||||||||||||||||||||||::||||||||
Db   542 GAGCTGCTGGAGGAGGATGGCCATGGGCCTTCCAGGAGGGCCCTA---GACCCAGGGCCCTTT   598

Qy   160 AspGlnGlySerProPheAlaGlyInGluGluLeuLeuAspAlaSerProGlyArgGlnIleAlaSerProTyr   179
           |||||||||||:::|||||||||||||||||||||||:::||||
Db   599 GACCAGGGCAGCCCCTTTGCCGGCCAGGAGGGTCAGCAACCCAGCCCTAC   658

Qy   180 TyrCysSerThrTyrGlyProGlyAlaProSerProGlySerSerAspValSerThrAla   199
           |:||| ::||:||||||||||||||||||||||||||||||||
Db   659 CACCCCGCAGCTGTGGCCGGCAGAGCCCCCTCCCTGGCAGCTCTGACCTCTCCACCGCA   718

Qy   200 ArgThrAlaThrProGlnSerSerHisAlaSerAspSerGlyGlySerAspValAspLeu   219
           ||:|||||||||||||||||||||||||||||||||||||||||||||||
Db   719 GGGGACTGGTGCTTCTCCGGAGCTCCCACTCCTCAGACTCCGGTGAAGGTGACGTGGACCTG   778

Qy   220 AspLeuThrGluSerLysValPheProArgAspThrTyrLysLysGlyGlu   239
           |||| ::|::||||||||:::|||||||||||||||:||
Db   779 GATCCCACTGAATGGCAACCTCTTCCCCAGCGATGGTTTCGTGACTGACAAGAAGGGGGAT   838

Qy   240 ProLysHisGlyLysArgGlyLysLeuSerLysGluTyrTrpAsp   259
           ||||||||||||||||||||||||||||||||
Db   839 CCCAAGCACGGGAAGCGGGAAAGCGGCCGCCTCCCAGACCCCGA   898

Qy   260 CysLeuGluGlyLysLeuLysSerHisAlaProAlaGlyThrHisLeuTrpGluPheIle   279
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   899 TGTCTGGAGGGCAAGAACAAGAGCCACGCACGCGCCCCAGAGGCGACCCACCTGTGGGAGTTCATC   958

Qy   280 ArgAspIleLeuHisProGlyLeuAsnGluGlyLeuMetLysSerTrpGluAsnArgHis   299
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   959 CGGGACATCCTCATCCACCCGGAGCTCAACGAGGGCCTCATGAAGTCGTGGGAGAATCGGCAT   1018

Qy   300 GluGlyValPheGlyLysPheLeuArgSerGluValAlaAlaGlnLeuTrpGlyLysLys   319
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1019 GAAGGCGTCTTCAAGTTCCTGCGCTCCGAGGTGGCCGCCCAACTATGGGGCCAAAAGAAA   1078

Qy   320 LysAsnSerAsnMetThrArgTyrGluLysLeuSerArgAlaMetArgTyrTyrLysArg   339
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1079 AAGAACAGCAACATGACCTACGAGAAGCTGAGCCGGGCCATGAGGTACTACAAACGG   1138

Qy   340 GluIleLeuGluArgValAspGlyArgArgLeuValTyrLysPheGlyLysAsnSerSer   359
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1139 GAGATCCTGGAACGGGTGGATGGCCGGCGGCTCGTCTACAAGTTTGGCAAAAACTCAAGC   1198

Qy   360 GlyTyrLysGluGluGluValGlyGluSerArgAsn   371
           |||||||||||||||||||||||||||||||||
Db   1199 GGCTGGAAGGAGGAAGAGGTTCTCCAGAGTCGGAAC   1234

Db   839   CCCAAGCACGGGAAGCGGGAAAGCGGCCGCCTCCCAGACCCCGA...

(lower continuation block)

RESULT 6
US-09-922-217-1105
Sequence 1105, Application US/09922217
Patent No. US2002007614A1
GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Stolk, John A.
APPLICANT: Wang, Tongtong
APPLICANT: Jiang, Yuqiu
APPLICANT: Smith, Carole Lynn
APPLICANT: King, Gordon E.
APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1105
; LENGTH: 1917
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-217-1105

Alignment Scores:
Pred. No.:
Score: 2.42e-172
                                1712.00   Length: 1917
Percent Similarity: 92.74%   Matches: 323
Percent Identity: 86.83%   Conservative: 22
Best Local Similarity: 86.25%   Mismatches: 25
Query Match: 10   Indels: 2
DB: Gaps: 2

US-08-978-217-16 (1-371) x US-09-922-217-1105 (1-1917)

Qy   1   MetAlaAlaThrCysGluIleSerAsnValPheSerAsnTyrPheAsnAlaMetTyrSer   20
           ||||||||||||||||||||||||||| ||:|||||||||||||||||||||||||
Db   122 ATGGCTGCAACCTGTGAGATTAGCAACAATTTTAGCAACTACTTCAGTCGGATGTACAGC   181

Qy   21   SerGluAspProThrLeuAlaProAlaProPro---ThrThrPheGlyThrGluAspLeu   39
           |||||||||:|||||||||||||||||| ::|||||||||||||

RESULT 7
US-09-925-301-207
; Sequence 207, Application US/09925301

; Patent No US20020523082A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 207
; LENGTH: 1996
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-301-207

Alignment Scores:
Pred. No.:
Score: 1712.00
Percent Similarity: 92.74%   Length: 1996
Percent Identity: 86.83%   Matches: 323
Best Local Similarity: 86.25%   Conservative: 22
Query Match: 10   Mismatches: 25
DB: Indels: 2
                                          Gaps: 2

US-08-978-217-16 (1-371) x US-09-925-301-207 (1-1996)

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Qy      1 MetAlaAlaThrCysGluIleSerAsnValPheSerAsnTyrPheAsnAlaMetTyrSer 20
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141 ATGGCTGCCAACCTGTGAGATTAGCAACATTTTTAGCAACTACTTTCAGTGCGATGTACAGC 200

Qy     21 SerGluAspProThrThrPheAlaProAlaProPro---ThrThrPheGlyThrGluAspLeu 39
            ::::||||||||||||||||||||||||||||||       :::|||||||||||
Db    201 TCGGAGGACTCCACCCTGGGCTCTGTCCGGCGTGCGCCACCTTTGGGCGGCCGATGACTTG 260

Qy     40 ValLeuThrLeuAsnAsnGlnIleMetThrLeuGluGlyProGlnLysAlaSerTrpThr 59
            |||||||||||||||::::||||||||||||||||||||||||||||
Db    261 GTACTGACCCTGAGCAACCCCCAGATGTCAATTGGAGGTACAGAGAAGGCCAGCTGGTTG 320

Qy     60 SerGluArgProGlnPheTrpSerLysThrGlnValLeuGluTrpIleSerTyrGlnVal 79
            |||||||||||||||||||||||||||||||||||||||||::::|||
Db    321 TCGGAGAGGCCCCAGTTCTGGTCGAAGACGCAGGTTCTGACTGGATCAGCTACCAAGTG 380

Qy     80 GluLysAsnLysTyrAspAlaSerSerIleAspProPheSerGlyProGlnLysAlaSer 99
            ||||||||||||||||||::::||||||||||
Db    381 GAGAAGAACAAGTACGACGCCAGCTCCATTGACCCCTTCTCAGGACCCCAGAAAGGCGCC 440
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... (alignment continues)

Left column

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Qy    220  AspLeuThrGluSerLysValPheProArgAspPheThrAspTyrLysLysGlyGlu  239
               ||  |||:::  :|
Db    798  GATCCCACTGATGGCCAAGCTCTTCCCAGCGATGGTTTTCGTGACTGCAAGAAGGGGGAT  857

Qy    240  ProLysHisGlyHisGlyArgGlyLysArgGlyProArgGlyLeuSerLysGluTyrTrpAsp  259
               ||||||||||||||||||||||
Db    858  CCCAAGCACGGGAAGGCGGAAACCGAGGCCCCGAAAGCTGAGCAAAGAGTACTGGGAC  917

Qy    260  CysLeuGluGlyLysLysSerGlyValHisAlaProAspArgGlyThrHisLeuThrPheIle  279
               ||| :||||||||||||||||| ||
Db    918  TGTCTCGAGGGCAAGAAGAGCAAGGCACCCGACCGGGGTTCATC  977

Qy    280  ArgAspIleLeuHisProGluLeuAsnGlyGlyLeuMetLysTrpGluAsnArgHis  299
               ||||||||||||||||||||||
Db    978  CGGGACAATCCCATCCACCCGGAGCTCAACGAGGGCCTCATGAAGTGGGAGAATCGGCAT  1037

Qy    300  GlyGlyValPheLysGluArgSerGluAlaValAlaGlnIleLeuTrpGlyTyrGlyLys  319
               |||||||||||||||||  |||||
Db    1038 GGAAGGCGTCTTCAAGTTCCTCGGGGCTGTGGCCCAACTACTACTACTACAAAGGG  1097

Qy    320  LysAsnSerAsnMetThrTyrGlyLysLysSerArgAlaMetArgTyrTyrTyrLysArg  339
               |||||||||||||||||||||||||||
Db    1098 AAGAACAGCAACATGACCTACGGAAAGTGAGCGGGGCCATGAGGTACTACTACAAAAGG  1157

Qy    340  GluIleLeuLeuArgValAspGlyArgArgLeuValTyrLysPheGlyLysAsnSerSer  359
               ||||||||||||||||||||||  |
Db    1158 GAGATCCTGCTGAGGGTGGATGGCCGGCGACTCGTCTACAAGTTTGGCAAAAACTCAAGC  1217

Qy    360  GlyTrpLysGlyGluGluGluValGlyGluSerArgAsn  371
               ||||||||||  |:::  ||
Db    1218 GGCTGGAAGGGAGGAGGAGGGGTTCTCCAGAGTCGGAAC  1253
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Right column

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US-08-978-217-16 (1-371) x US-10-025-380-853 (1-626)

Qy    52   GlyProGluLysAlaSerTrpThrSerGluArgProGlnPheThrSerLysThrGlnVal  71
               ||  ::||||||||||||||||||
Db    624  GGTACAGAGAAGGCCAGCTGGACTAGAGAGAGGCCCCAGTTCTCGGTCAAGACCCAGGTT  565

Qy    72   LeuGluTrpIleSerTyrGlnValGlyLysAsnGlyAsnLysTyrAsnAlaSerSerIleAspPhe  91
               ||:::  ||||||||||:::  ||  ||
Db    564  CTGGAACTGGATCAGCTACCAAGTGGGAGAAGAAGTACGACGCCATTGACTTC  505

Qy    92   SerArgCysAsnAspTyrAlaThrLeuCysSerSerCysAlaLeuGluGluLeuArgGlu  111
               ||||||||||||||||||||||||||||
Db    504  TCACGGATGTGACATGGGCGGCCACCCTCGAATTGTCCCCTTGAGGAGCTCGGTCTG  445

Qy    112  ValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgLeuThrSerAsnSer  131
               ||||||||||||||||||:::  ||||||
Db    444  GTCTTTGGGCCCTTCGGGGACCAACTCCATGCCCAGCTGCGGCTGACCTCCAACTCTCCAGCTCT  385

Qy    132  SerAspGluLeuSerTrpIleLeuGluLeuLeuAspLysProPheAlaGlnGlnLeuLeuAsp  151
               ||||||||||||||||||||||:::  ||||
Db    384  TCTGATGAGCTCAGTTGGATCATTGAGCTGCTGGACAAGCCATTCGCCCAGCAGCTGCTGGAC  325

Qy    152  SerLeuGlyAsnProPheGluAspGlyGlySerProPheAlaGlnAsnLeuLeuAsp  171
               ||||||||||||||||||::: |
Db    324  GCCCTA---GACCCAGGGCGCCTTTGACCAGGCGACAGCCCCTTTGCCCAGGAGCTGCTGGAC  268

Qy    172  AspGlyArgGlnAlaSerProTyrTyrCysSerThrTyrGlyProGlyAlaProSerPro  191
               ||||||||||:::  |||
Db    267  GACGGTCAGCAAGCCCAGGCCCCTACACCCCGGGCCGAGCGTGGGGCGCAGGAGCTGGGCTCCC  208

Qy    192  GlySerSerAspValSerThrAlaArgThrAlaThrProGlnSerSerHisAlaSerAsp  211
               |||||||:::  ||||||||||
Db    207  GGCAGCCTCTGACGGTCTCCACCGCAGGGACTGGTGCTTCTCGGACTCCTCAGAC  148

Qy    212  SerGlyGlySerAspValAspLeuAspLeuHisGluSerLysValPheGlyAspAspAsp  231
               ||:::  ||||||||||
Db    147  TCCGGTGGAAGTGACGTGGACCTGGACCTCCATGAGTCCAAGGTCTTCGGAGACGATGGT  88

Qy    232  PheThrAspTyrLysLysGlyLysProLysHisGlyHisGlyLysGlyLysArgGlyProArg  251
               |||  |||||||||||||:::  ||||
Db    87   TTTCGTGACTGCAAGAAGGGGGATCCCAAGCACGGGAAGGCGGAAACGAGGCCCCCGA  28

Qy    252  LysLeuSerLysGluTyrTrpAspCys  260
               |||||||||||||||||
Db    27   AAGCTGAGCAAAGAGTACTGGGACTGT  1
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Alignment Scores:
Pred. No.:
Score:                      8.66e-90
Percent Similarity:         928.50
Best Local Similarity:      90.91%
Query Match:                83.25%
DB:                         46.78%
                            9
Length:                     626
Matches:                    174
Conservative:               16
Mismatches:                 18
Indels:                     1
Gaps:                       1
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Left column

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RESULT 10
US-09-833-263-853/c
; Sequence 853, Application US/09833263
; Patent No. US2002011054721
; GENERAL INFORMATION:
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Stolk, John A.
; APPLICANT: Meagher, Madeleine J.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C12
; CURRENT APPLICATION NUMBER: US/09/833,263
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 1093
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-217-853

Alignment Scores:
Pred. No.:
Score: 928.50
Percent Similarity: 90.91%
Best Local Similarity: 83.25%
Query Match: 10

Length: 626
Matches: 174
Conservative: 16
Mismatches: 18
Indels: 1
Gaps: 1

US-08-978-217-16 (1-371) x US-09-922-217-853 (1-626)

```
Qy   52 GlyProGlyLysAlaSerTrpThrSerGluArgProGlnPheTrpSerLysThrGlnVal  71
Db  624 GGTACAGAGAAGGCCAGCCTGGTTGGGGGACAGAGCCCAGTTCTGGTTCGAAGACGCAGGTT 565

Qy   72 LeuGluTrpIleSerTyrArgGlnValGlyLysAsnLysTyrAspAlaSerSerIleAspPhe  91
Db  564 CTGGACTGGATCAGCTACCAAGTGGGAGAAGAACAAGTACGACGCGCCATTGACTTC      505

Qy   92 SerArgCysAsnMetAspGlyAlaThrLeuCysSerSerCysAlaLeuGluGluLeuArgLeu 111
Db  504 TCACGATGTGACATGGATGGCGCCACCCTTGCAATTGTCCCTTGAGGAGCTGCGTCTG      445

Qy  112 ValPheGlyProLeuGlyAspGlnIleuHisAlaGlnIleLeuArgAspLeuThrSerAsnSer 131
Db  444 GTCTTTGGGCCTCTGGGGGACCAACTCCATGCCCAGATCCTGCGAGACCTCACTTCCAGCTCT 385

Qy  132 SerAspGluLeuSerTrpIleIleGluLeuGluGlyMetSerPheGlnGlu 151
Db  384 TCTGAATGAGCTCAGTTGGATCATTGAGCTGGAGGGCATGGCCTTCCAGGAG 325

Qy  152 SerLeuGlyAspLeuGlyProPheAspGlnGlySerProPheAlaGlnGluLeuLeuAsp 171
Db  324 GCCCTA---GACCCAGGGCCCTTTGACCAGGGCAGCCCCTTTGCCCAGGAGCTGCTTGGAC 268

Qy  172 AspGlyArgGlnAlaSerProTyrTyrCysSerThrTyrGlyProGlyAlaProSerPro 191
Db  267 GACGGTCAGCAAGCCAGCCCCTACCACTGTGGCACAGCCCCCTCCCCC         208

Qy  192 GlySerSerAspValSerThrAlaArgThrAlaThrProGlnSerSerHisAlaSerAsp 211
Db  207 GGCAGCTCTGACGTCTCCACCGCAGGGACTGGGTGCTTCTCGGAGCTCCACTCCTCAGAC 148

Qy  212 SerGlyGlySerAspValAspLeuAspLeuThrGluSerIleLysValPheProArgAspAsp 231
Db  147 TCCGGTGGAAGTGACGTGGACCTGGACCTCTTCCCCAGCGATGGT       88

Qy  232 PheThrAspTyrLysLysGlyLeuProLysHisGlyLysLysGlyArgGlyArgProArg 251
Db   87 TTTCGTGACTGCAAGAAGGGGGATCCCAAGCACGGGAAGCCGGAAAACGAGGGCCCCGGA 28

Qy  252 LysLeuSerLysGluTyrTrpAspCys 260
Db   27 AAGCTGAGCAAAGAGTACTGGGACTGT 1
```

Right column

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; SOFTWARE: FastSEQ for Windows Version 3.0
; TYPE: DNA
; SEQ ID NO 853
; LENGTH: 626
; ORGANISM: Homo sapien
US-09-833-263-853
```

; TYPE: DNA
; ORGANISM: Homo sapien
US-09-833-263-853

Alignment Scores:
Pred. No.:
Score: 928.50
Percent Similarity: 90.91%
Best Local Similarity: 83.25%
Query Match: 10

Length: 626
Matches: 174
Conservative: 16
Mismatches: 18
Indels: 1
Gaps: 1

US-08-978-217-16 (1-371) x US-09-833-263-853 (1-626)

```
Qy   52 GlyProGlyLysAlaSerTrpThrSerGluArgProGlnPheTrpSerLysThrGlnVal  71
Db  624 GGTACAGAGAAGGCCAGCCTGGTTGGGGGACAGAGCCCAGTTCTGGTTCGAAGACGCAGGTT 565

Qy   72 LeuGluTrpIleSerTyrArgGlnValGlyLysAsnLysTyrAspAlaSerSerIleAspPhe  91
Db  564 CTGGACTGGATCAGCTACCAAGTGGGAGAAGAACAAGTACGACGCGCCATTGACTTC      505

Qy   92 SerArgCysAsnMetAspGlyAlaThrLeuCysSerSerCysAlaLeuGluGluLeuArgLeu 111
Db  504 TCACGATGTGACATGGATGGCGCCACCCTTGCAATTGTCCCTTGAGGAGCTGCGTCTG      445

Qy  112 ValPheGlyProLeuGlyAspGlnIleuHisAlaGlnIleLeuArgAspLeuThrSerAsnSer 131
Db  444 GTCTTTGGGCCTCTGGGGGACCAACTCCATGCCCAGATCCTGCGAGACCTCACTTCCAGCTCT 385

Qy  132 SerAspGluLeuSerTrpIleIleGluLeuGluGlyMetSerPheGlnGlu 151
Db  384 TCTGAATGAGCTCAGTTGGATCATTGAGCTGGAGGGCATGGCCTTCCAGGAG 325

Qy  152 SerLeuGlyAspLeuGlyProPheAspGlnGlySerProPheAlaGlnGluLeuLeuAsp 171
Db  324 GCCCTA---GACCCAGGGCCCTTTGACCAGGGCAGCCCCTTTGCCCAGGAGCTGCTTGGAC 268

Qy  172 AspGlyArgGlnAlaSerProTyrTyrCysSerThrTyrGlyProGlyAlaProSerPro 191
Db  267 GACGGTCAGCAAGCCAGCCCCTACCACTGTGGCACAGCCCCCTCCCCC         208

Qy  192 GlySerSerAspValSerThrAlaArgThrAlaThrProGlnSerSerHisAlaSerAsp 211
Db  207 GGCAGCTCTGACGTCTCCACCGCAGGGACTGGGTGCTTCTCGGAGCTCCACTCCTCAGAC 148

Qy  212 SerGlyGlySerAspValAspLeuAspLeuThrGluSerIleLysValPheProArgAspAsp 231
Db  147 TCCGGTGGAAGTGACGTGGACCTGGACCTCTTCCCCAGCGATGGT       88

Qy  232 PheThrAspTyrLysLysGlyLeuProLysHisGlyLysLysGlyArgGlyArgProArg 251
Db   87 TTTCGTGACTGCAAGAAGGGGGATCCCAAGCACGGGAAGCCGGAAAACGAGGGCCCCGGA 28

Qy  252 LysLeuSerLysGluTyrTrpAspCys 260
Db   27 AAGCTGAGCAAAGAGTACTGGGACTGT 1
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RESULT 11
US-10-025-380-944/c
; Sequence 944, Application US/10025380
; Publication No. US2002018219A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
```

RESULT 12

; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025,380
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 1129
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 944
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-025-380-944

Alignment Scores:
Pred. No.:
Score: 9.24e-80
Percent Similarity: 833.50   Length: 563
Best Local Similarity: 91.49%   Matches: 157
Query Match: 83.51%   Conservative: 15
                        41.99%   Mismatches: 15
                        9   Indels: 1
                                        Gaps: 1

US-08-978-217-16 (1-371) x US-10-025-380-944 (1-563)

Qy   73 GluTrpIleSerTyrGlnValGlyLysAsnLysTyrArgAlaSerIleAspPheSer 92
          :|||||||||||||||||||||||||||||||||||||||| :||||||||||||||
Db 562 GACTGGATCAGCTACCAAGTGGAAGAACAACAAGTACGACGCCAAGCGCCATTGACTTCTCA 503

Qy 113 PheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThrSerAsnSerSer 132
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 442 TTTGGGCCCTCTGGGGACCAAACTCCATCCCACGCTGCGAGACCTCACTTCACCTCTTCT 383

Qy 133 AspGluLeuSerTrpIleIleGluLeuLeuGluLysAspGlyMetSerPheGlnGluSer 152
          :||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 382 GATGAGCTCAGTTGGATCAATTGAGCTGCTGGAGAAGGATGGCATGAGCCTTCCAGGAGGCC 323

Qy 153 LeuGlyAspLeuGlyProPheAspGlnGlySerProPheAlaGlnGluLeuLeuAspAsp 172
         ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 322 CTA---GACCCAGGGCCCTTTGACCAGGGCAGCCCCTTTGCCCAGGAGGTGCTGGACGAC 266

Qy 173 GlyArgGlnAlaSerProThrTyrCysSerThrTyrArgGlyTyrCysSerProGly 192
         |||||||||||||||||||| :||||||||||||||||||||||||||||||||||
Db 265 GGTCAGCAAGCCAGCCCCTACCACCCGCAGCGTGTGCGCAGAGGGCGCCCCTCCCCGGC 206

Qy 193 SerSerAspValSerThrAlaAlaArgThrAlaThrProGlnSerSerHisAlaSerSer 212
         ||||||||||||||||||| :|||||||||||||||||||||||||||||||||||||
Db 205 AGCTCTGACGTCTCCACCGCGGCTAGGACTGCTACCCCACTCCAGCTCCTTCT 146

Qy 213 GlyGlySerAspValAspLeuAspLeuValPheProArgAspAspPhe 232
         ||||||||||||||||||||||||||||||||||||||||:|||||||
Db 145 GGTGGAAGTGACGTGGACCTGGATCCACTGATGGCCAAGCTCTCCCCAGCCGATGGTTTT 86

Qy 233 ThrAspTyrArgLysGlyGluProLysHisGlyLysSerArgGlyArgProArgLys 252
         ||| :|||||||||||||||||||||:||||||||||||||||||||||||||||||
Db   85 CGTGACTGCACAGAAGGGGGATCCCAAGCACGGGAAACAGAGGCCGCGGCCCCGGAAAG 26

Qy 253 LeuSerLysGluTyrTrpAspCys 260
         ||||||||||||||||||||||||
Db   25 CTGAGCAAAGAGTACTGGGACTGT 2

US-09-922-217-944/c
; Sequence 944, Application US/09922217
; Patent No. US20020076414A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole Lynn
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C13
; CURRENT APPLICATION NUMBER: US/09/922,217
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 944
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-922-217-944

Alignment Scores:
Pred. No.:
Score: 9.24e-80
Percent Similarity: 833.50   Length: 563
Best Local Similarity: 91.49%   Matches: 157
Query Match: 83.51%   Conservative: 15
                        41.99%   Mismatches: 15
                        10   Indels: 1
                                        Gaps: 1

US-08-978-217-16 (1-371) x US-09-922-217-944 (1-563)

Qy   73 GluTrpIleSerTyrGlnValGlyLysAsnLysTyrArgAlaSerIleAspPheSer 92
          :|||||||||||||||||||||||||||||||||||||||| :||||||||||||||
Db 562 GACTGGATCAGCTACCAAGTGGAAGAACAACAAGTACGACGCCAAGCGCCATTGACTTCTCA 503

Qy 113 PheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThrSerAsnSerSer 132
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 442 TTTGGGCCCTCTGGGGACCAAACTCCATCCCACGCTGCGAGACCTCACTTCACCTCTTCT 383

Qy 133 AspGluLeuSerTrpIleIleGluLeuLeuGluLysAspGlyMetSerPheGlnGluSer 152
          :||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 382 GATGAGCTCAGTTGGATCAATTGAGCTGCTGGAGAAGGATGGCATGAGCCTTCCAGGAGGCC 323

Qy 113 PheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuSerProPheAlaGln 132
         ||||||||||||||||||| :||||||||||||||||||||||||||||||||||||||
Db 442 TTTGGGCCCTCTGGGGACCAAACTCCATCCCACGCTGCGAGACCTCAGT 383

Qy 153 LeuGlyAspLeuGlyProPheAspGlnGlySerProPheAlaGlnGluLeuLeuAspAsp 172
         ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 442 CTA---GACCCAGGGCCCTTTGACCAGGGCAGCCCCTTTGCCCAGGAGGTGCTGGACGAC 266

Qy 133 AspGluLeuSerTrpIleIleGluLeuLeuGluLysAspGlyMetSerPheGlnGluSer 152
          :|||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db 442 GATGAGCTCAGTTGGATCAATTGAGCTGCTGGAGAAGGATGGCATGAGCCTTCCAGGAGGCC 323

Qy 153 LeuGlyAspLeuGlyProPheAspGlnGlySerProPheAlaGlnGluLeuLeuAspAsp 172
         ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 442 CTA---GACCCAGGGCCCTTTGACCAGGGCAGCCCCTTTGCCCAGGAGGTGCTGGACGAC 266

Qy 173 GlyArgGlnAlaSerProThrTyrCysSerThrTyrArgGlyTyrCysSerProGly 192
         |||||||||||||||||||| :|||||||||||||||||||||||||||||||||||
Db 265 GGTCAGCAAGCCAGCCCCTACCACCCGCAGCGTGTGCGCAGAGGGCGCCCCTCCCCGGC 206

Qy 193 SerSerAspValSerThrAlaAlaArgThrAlaThrProGlnSerSerHisAlaSerSer 212
         ||||||||||||||||||| :|||||||||||||||||||||||||||||||||||||
Db 205 AGCTCTGACGTCTCCACCGCGGCTAGGACTGCTACCCCACTCCAGCTCCTTCT 146

Qy 213 GlyGlySerAspValAspLeuAspLeuValPheProArgAspAspPhe 232
         ||||||||||||||||||||||||||||||||||||||||:|||||||
Db 145 GGTGGAAGTGACGTGGACCTGGATCCACTGATGGCCAAGCTCTCCCCAGCCGATGGTTTT 86

Qy 233 ThrAspTyrArgLysGlyGluProLysHisGlyLysSerArgGlyArgProArgLys 252
         ||| :|||||||||||||||||||||:||||||||||||||||||||||||||||||
Db 145 CGTGACTGCACAGAAGGGGGATCCCAAGCACGGGAAACAGAGGCCGCGGCCCCGGAAAG 26

```
Db    85 CGTGACTGCAAGAAGAGGGGGATCCCAAGCACGGGAAGCGGGAAACGAGGCCCGGCCCCGAAAG    26

Qy   253 LeuSerLysGluTyrTrpAspCys 260
Db    25 CTGAGCAAAGAGTACTGGGACTGT  2
```

RESULT 13
US-09-833-263-944/c

; Sequence 944, Application US/09833263
; Patent No. US2002011054701A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Stolk, John A.
; APPLICANT: Meagher, Madeleine J.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471CI2
; CURRENT APPLICATION NUMBER: US/09/833,263
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 944
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-833-263-944

Alignment Scores:
Pred. No.:
Score: 9.24e-80
Percent Similarity: 833.50   Length: 563
Best Local Similarity: 91.49%   Matches: 157
Query Match: 83.51%   Conservative: 15
DB: 41.99%   Mismatches: 15
                                10   Indels: 1
                                                Gaps: 1

US-08-978-217-16 (1-371) x US-09-833-263-944 (1-563)

Qy   73 GluTrpIleSerTyrGlnValGlyLysAsnLysTyrAspAlaSerIleAspPheSer 92
         ||| |||||:||:|||||||||||||||||:|||:||||||||:||::||||
Db   562 GACTGGATCAGCTACCAAGTGGGAAAGAACAAGTACGACGGGAAGCCCCATTGACTTCTCA 503

Qy   93 ArgCysAsnMetAspGlyAlaThrLeuCysSerCysAlaLeuGluGluLeuArgLeuVal 112
         ||||||| ||||||:|||:||:||||:|||||||||:|||||||||:||||||||:||:
Db   502 CGATGTGACAATGGATGGGCGCCACCCTCTGCAATTGTGCCCTTGAGGAGTCTGCGGTC 443

Qy   113 PheGlyProLeuGlyAspGlyHisLeuHisLeuArgAspLeuThrSerAsnSerSer 132
         |||||||||||||||||||||:||||| |||||||||||||||||:|||:|||:||
Db   442 TTTGGGCCCTCTGGGGGACCAACTCCATGCCGAGACCTCACTTCCAGCTCTTCT 383

Qy   133 AspGluLeuSerTrpIleIleGluLeuVaLLysGlyMetSerPheGlnGlySer 152
         |||||||||||:||||||||:|||||:||:|||::::||
Db   382 GATGAGCTCAGTTGGATCAATTGAGCTGGCTGAAGAGGGATGGCCTTCCAGGAGGCC 323

Qy   153 LeuGlyAspLeuGlyProPheAspProThrProAlaGlnGluLeuLeuLeuAspAsp 172
         |||||:|||:||||:|||||||||:|||:|||:|||||:|||||||:|||||||
Db   322 CTA---GACCCAGGGCCCTTGACCAGGGCAGCCCCTTTGCCCCAGGAGCTGCTGCTGGACGAC 266

Qy   173 GlyArgGlnAlaSerProTyrTyrCysSerThrThrGlyProGlyValAlaProSerProGly 192
         |||:::|||||| |||||||||||:|||||:::|||||||||:||::|
Db   265 GGTCAGCAACCCAGCCCCTACCACCCCGGAGCTGTGGCCAGGAGCCCCCCCGGC 206

Qy   193 SerSerAspValSerThrAlaArgThrAlaThrProGlnSerSerHisAlaSerAspSer 212
         |||||||||||:||||:|||:||:|||::|||:||::
Db   205 AGCTCTGACGTCTCCACCGCAGGGACGGCTGCCACTCCTCAGACTCC 146

Qy   213 GlyGlyLysSerAspValAspLeuAspLeuAspGlyLeuGluSerLysGluSerAsnMet 232
         |||:||:|||||||||||:|||||||||||||:::||||||||
Db   145 GGTGGAAGTGACGTGGACCTGGACCTCGATCCCACTGATGGTTTT 86

Qy   233 ThrAspTyrLysGlyGluProLysHisGlyLysArgGlyIleArgProArgLys 252
         |||||||:|||::|:|||||||||:||::||||:||||||:
Db   85 CGTGACTGCAAGAAGAGGGGGATCCCAAGCACGGGAAGCGGGAAACGAGGCCCGGCCCCGAAAG 26
```

```
Qy   253 LeuSerLysGluTyrTrpAspCys 260
         |||||||||||||||||||||||
Db    25 CTGAGCAAAGAGTACTGGGACTGT 2
```

RESULT 14
US-10-076-622-282

; Sequence 282, Application US/10076622
; Publication No. US20030023036A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470CI1
; CURRENT APPLICATION NUMBER: US/10/076,622
; CURRENT FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 282
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-076-622-282

Alignment Scores:
Pred. No.:
Score: 1.36e-76
Percent Similarity: 803.00   Length: 502
Best Local Similarity: 93.33%   Matches: 149
Query Match: 90.30%   Conservative: 5
DB: 40.45%   Mismatches: 11
                                9   Indels: 0
                                                Gaps: 0

US-08-978-217-16 (1-371) x US-10-076-622-282 (1-502)

Qy   185 GlyProGlyAlaProSerProGlySerSerAspValSerThrAlaArgThrAlaThrPro 204
         ||| |||||||||||||||||||||||||||||||||||||
Db   6 GGGCGCAGGAGCGCCCCTCCCCCGGGCAGCTCTGACGTCTCCACCGCAGGGGACTGGCTGCTTCT 65

Qy   205 GlnSerSerHisAlaSerAspSerGlyGlyLysSerAspValAspLeuAspLeuAspGlySer 224
         |||||||:|||| ||||||||||:::|||||||:|:::
Db   66 CGGAGGTCCCACTCCTCAGACTCCGGTGGAAGTGACGTGGACCTGGATCCCACTGATGGC 125

Qy   225 LysValPheProArgAspAspPheThrAspTyrLysGlyGlyHisGlyLys 244
         ||||:||||||||||||||:::|||::||||
Db   126 AAGCTCTTCCCCAGCGATGGTTTTCGTGACTGCAAGAAGACGGGAAAG 185

Qy   245 ArgLysArgGlyArgProArgLysLeuSerLysGluTyrTrpAspCysLeuGluGlyLys 264
         |||:||||||||:|||||||||:||||||||||:|||||:|||||||||||:|||
Db   186 CGGAAACGAGGCCCGGCCCCGAAAGCTGAGCAAAGAGTACTGGGACTGTCTCGAGGGCAAG 245

Qy   265 LysSerLysHisAlaProArgGlyThrHisLeuTrpGluPheIleArgAspIleLeuIle 284
         ||||||||:|||||||||||||||:|||||:||||||||::|||||||
Db   246 AAGAGCAAGCACGCGCCCAGAGGCACCCACCTGTGGGAGTTCATCCGGGACATCCTCATC 305

Qy   285 HisProGluLeuAsnGluLeuTyrLeuMetLysTrpGlyAsnArgHisGlyGlyValPheLys 304
         ||||||:|||||::|||||||||||||:|||||:|||||||||:|||||||||||
Db   306 CACCCGGAGCTCAACGAGGGCCTCAGAAGTGGGAGAATCCGCATGAAGGCCGTCTTCAAG 365

Qy   305 PheLeuArgSerGlnValAlaValAlaGlnLeuTrpGlyGlnValGlyLysGlyAsnSerAsnMet 324
         |||:||:|:::||||||:|||:|||||:|||:|::::|||::||:
Db   366 TTCCTGCGCTCCCGAGCGGTCGTGGCCCAACTATGGGGCCCAACGAGCAACATG 425

Qy   325 ThrTyrGluLysSerLeuSerArgAlaMetArgTyrTyrLysArgGluLysGluArg 344
         |||||::|::||||||:|||:||::|||::||||||||||||||||:||||
Db   426 ACCTACGAGAAGAGCTGAGCCCGGCCCCGCCCATGAGGTACTACAAACGGGAGAAGGAGATCCGG 485

Qy   345 ValAspGlyArgArg 349
         ||||||:|||||
Db   486 GTGGATGGCCGGCGA 500
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RESULT 15

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US-09-604-287A-282
; Sequence 282, Application US/09604287A
; Patent No. US20020064872A1
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Yuqiu
;  APPLICANT: Dillon, Davin C.
;  APPLICANT: Mitcham, Jennifer L.
;  APPLICANT: Xu, Jiangchun
;  APPLICANT: Harlocker, Susan L.
;  APPLICANT: Hepler, William T.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.470C7
;  CURRENT APPLICATION NUMBER: US/09/604,287A
;  CURRENT FILING DATE:  2000-06-22
;  NUMBER OF SEQ ID NOS: 489
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 282
;  LENGTH: 502
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-09-604-287A-282

Alignment Scores:
Pred. No.:
Score:                  1.36e-76       Length:            502
Percent Similarity:     803.00         Matches:           149
Best Local Similarity:  93.33%         Conservative:        5
Query Match:            90.30%         Mismatches:         11
DB:                     40.45%         Indels:              0
                        10             Gaps:                0

US-08-978-217-16 (1-371) x US-09-604-287A-282 (1-502)

Qy   185 GlyProGlyAlaProSerProGlySerSerAspValSerThrAlaArgThrAlaThrPro 204
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     6 GGCGCAGGAGCCCCCTCCCCCGGCAGCTTCTGACGTCTTCCACCCGCAGGGACTGGTGCTTCT 65

Qy   205 GlnSerSerHisAlaSerAspSerGlyGlySerAspValAspLeuAspLeuThrGluSer 224
         ::||||||||||||||:::|||||||||||||||||||||||||||||||:::
Db    66 CGGAGCTCCCACTCCTCCAGATCTCCGGTGGAAGTGACGTGGACCTGGATCCCACTGATGGC 125

Qy   225 LysValPheProArgAspAspPheThrArgTyrLysGlyGlyHisHisGlyLys 244
         |||:::||||  ||| |||||||||||||||||:|||||||||||||||
Db   126 AAGCTCTTCCCCAGCGATGGTTTTCGTGACTCGCAAGAAGGGGGATCCCAAGCACGGGAAG 185

Qy   245 ArgLysArgGlyArgProArgGlySerLeuSerLysGluTyrTrpAspCysLeuGluGlyLys 264
         |||||||:|||||||||||||||||||||||||||||||||||||||
Db   186 CGGAAACGAGGCCGGCCCCGAAAGCTGAGCAAAGAGTACTGGGACTGTCTCCGAGGGCAAG 245

Qy   265 LysSerLysHisAlaProArgGlyThrHisLeuTrpGluPheArgAspIleLeuIle 284
         |||||||||||| |||||||| |:||:||||| |||||||||||||||
Db   246 AAGAGCAAGCACGGCGCCCAGAGGGCACCACCCTGTGGGAGTTCATCCCGGACATCCTCATC 305

Qy   285 HisProGluLeuAsnGluGlyLeuMetLysTrpIleAsnArgHisGlnGlyValPheLys 304
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   306 CACCCGGAGCTCAACGAGGGCCTCATGAAGTGGGAGAATCGGCATGAAGGGGTCTTCAAG 365

Qy   305 PheLeuArgSerGluAlaValAlaGlnLeuTrpGlyGlnLysLysLysAsnSerAsnMet 324
         ||||||||| |||||||||||||||||||||||||||||||||||||||
Db   366 TTCCTGCGCTCCGAGGCTGTGGCCCAACTATGGGGCCAAAAGAAAAAGAACAGCAACATG 425

Qy   325 ThrTyrGlyLysSerArgAlaMetArgTyrTyrLysArgGlnIleLeuGluArg 344
         ||||||||||||||||||||||||||||||||||||||||||||||
Db   426 ACCTACGGAGAAGCTGACCGCGGGGCCATGAGGTACTACTACAAACGGGAGAATCCTGGAACGG 485

Qy   345 ValAspGlyArgArg 349
         ||||||||||||
Db   486 GTGGATGGCCGGCGA 500
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Search completed: March 16, 2003, 03:36:23
Job time : 112.105 secs